

# Replacement Sheet

## Gene III leader sequence in KO7 helper phage

SEQ ID NO. 1	GTG AAA AAA TTA TTA TTC GCA ATT CCT TTA GTT GTT CCT TTC TAT TCT CAC TCC GCT
SEQ ID NO. 2	V K K L L L F A I P L V V P F Y S H S A

## Gene III leader sequence in KO7kpn helper phage

	KpnI
SEQ ID. NO. 3	GTG AAA AAA TTA TTA TTC GCA ATT CCT TTA GTG GTA CCT TTC TAT TCT CAC TCC GCT
SEQ ID. NO. 2	V K K L L L F A I P L V V P F Y S H S A



Fig. 3B



# Replacement Sheet

## GR2-Myc domain coding sequence in GM-UltraHelper phage genome

SEQ ID. NO. 4  
KpnI Gene III leader GR2  
---TTAGTGGTACCTTTCTATTCTCACTCCGCT ACATCCCGCCTGGAGGGCCTACAGTCAGAAAAACCATCGCCTGCCGA

SEQ ID. NO. 5  
- L V V P F Y S H S A T S R L E G L Q S E N H R L R

NotI  
ATGAAGATCACAGAGCTGGATAAAGACTTGAAGAGGTCAACCATGCAGCTGCAGGACGTCGGAGGTTGC GCGGCCGCA  
M K I T E L D K D L E E V T M Q L Q D V G G C A A A

Myc-tag BglII Gene III  
GAACAAAACTCATCTCAGAAGAGGATCTG AGATCTGGAGGCGGT ACTGTTGAAAAGTTGTTTAGCAAAA---  
E Q K L I S E E D L R S G G G T V E S C L A K -

Fig. 5B



## Replacement Sheet

Trypsin cleavage sites at GR2-Myc domain on GM-UltraHelper phage

SEQ ID NO. 6

### GR2 domain

T S R **▲** L E G L Q S E N H R **▲** L R M K **▲** I T E L D K **▲** D L E E V

### *Myc-tag*

T M Q L Q D V G G C A A E Q K **▲** L I S E E D L R S G G G

Fig. 5C



SEQ ID NO. 7

GCGCAACGCAATTAATGTGAGTTAGCTCACTAATTAGCACCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGAATTTGTGAGCGGATACAATTTACCGGTTCTTTTAAGGAGGA  
 ATTAAAAAAGAAATCCTATTGCTACGGCAGCGCTGGATTGTATTACTCGCGGCCACCGCGGCCATGCGGCCCTCTAGAGCGCCGCTGGAGGTGAGAGAGTCCCGGCTG  
 TTGCGAGAGGAGAAACCGTGAATCGAAGAGGAGGGTGCTCTGAATCGGCCATCAACTCCAGTCTGTAGGAGTTGTAGATCTTTATCCATACGAAGTACCCAGACTA  
 CCGCAGAGGTATCATCACTATCCACTAATGAGTCGACCTGACCAATTTCCGCCATTAATGAGTCGTATTACATCTACTGCGGCTGCTTTTACACAGTCGTCTGATGGAACCAACCTTGGCGTT  
 ACCCAACTTAATCGCCTTCGACGACATCCCTTTTCGCGACATCCCTTTTCGCGATAGAGGCGCGACCGATCGCCCTTCCACAGTGAATGCGCAATGGGACGCGCCCTGTAG  
 CCGCGCAATTAAGCGCGCGGGTGTGGTTACGCGAGCGTGAACCTTACCTTTCGCGATAGAGGCGCGCTTTCGCTTTCTTCCCTTCTTCCGCCACGTTTCGCGGCTTTCCCC  
 GTCAAGCTTAATTCGGGGCTCCCTTTAGGGTTCGATTTAGTGTCTTACGCGACCTCGACCCCAAAAACCTTGATTAGSGTGATGTTCACTGAGTGTGGCCATCGCCCTGATTAGACGGCTTTT  
 CGGCTTTTGACGTTGGAGTCCAGCTTCTTTAATAGTGACCTCTGTTTCCAAATGGAACCACTCAACCCATCTATCTCGTCTATTCTTTGATTATTAAGGATTTTGGCGATTTGGCGTATTAT  
 GTTAAAAAATAGCTGATTTACAAAANAATTAACCGGAATTTTACAAAATTAATAAATTAATGAAAAAGGAAGAGTATCAGTATTCAACATTTCCGTGCGCCCTTATTTGTTTATTTCTTAAT  
 ACATTCAAATATGTATCGCTCATGAGACAATTAACCCCTGATAAATGCTTCAATTAATAATGAAAAAGGAAGAGTATCAGTATTCAACATTTCCGTGCGCCCTTATTTGTTTATTTCTTAAT  
 GCGCTCTCTGTTTTTGTCTCACCGAGAACCGCTGTGAAATAAAGATGCTGAAGATCAGTTGGTGACGAGTGGGTTACATCGAACCTGGAATCAACAGGGTGAAGATCCTTGAAGAGTTTTCGC  
 CCCGAAGAACGTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGGGTATTATCCCGTATTGACCGCGCAGAGCAAACTCGCTCGCCGATACACTATTCTCAGAATGACTGTGT  
 TGAGTACTCACCACTACAGAAAACATCTTACGGATGGCATGACATGACATGAGAAATTTATGCACTGTGCTCCATPACCATGAGTGAATACACTTCGGCCCACTTACTTCTGACAACTGCGGAGC  
 CAGAAAGCTAACCGTTTTTTCGAACAATCGGGGATCATGTAACTGCTGTTGGGAACCGGAGCTGAATGAGCCATACCAACAGCAGCGTGCACACCACTGCCTGATGCACAATG  
 GCGAACACCTTGCCCAAACTATTAACTGCGNACTACTTACTCTAGCTTCCCGGCACAAATTAATACATGATGAGCGGATAAAGTAAAGTTCAGAGCACTCTCGCTCGGCCCTTCCGGCTGG  
 CTGCTTTATGCTGATAAATCTGGACCGGTGACGTGGGTCTCGCGGTATCATTCGACGACTGGGCGCAGATGTTAAGCCCTCCCGTATCGTAGTATCTACAGCAGCGGGAGTCAAGCAACTA  
 TGGATGAACGAATAGACAGATCGCTGAGATAGTGGCTCACTGATTAAAGCATTTGTTAACTCTCAGACCAAGTTTAACTCATATATACTTTAGATTGATTTAAAACTTCAATTTTAAATTTAAAAAG  
 ATCTAGGTGGAAGTCTTTTGATTAATCTCATGACCAAAATCCCTTAACTGAGTTTTCGTTTCACCTGAGGCTCAGACCCGCTAGAAAAGATCAAAAGGATCTTCTTGAGATCTTTTTTCTTGCG  
 CGTAACTCTGCTTGAAACAAAACCAACCGCTACACCGGTGTTTGTTCGCGGATCAAGAGCTACCACTTTTTCGGAAGTAACTGSCCTTCAGCAGGCGGATACCAAAATCCTG  
 TTTGACTTACTGTAGCCGTATTAGCGCCACACTTCAAGAACTCTGATGCAACCGCTCATACACTCGCTCTGTCTAATCTGTATTACCACTGGCTGCTGCCAGTGGCAATAGTCTGTCTTACACCGG  
 TTGGACTCAAGACGATAGTTACCGGATTAAGCGACCGGTTCGGCTGAACGGGGGTTTCGTGCACACACCCACGTTTGGAGCGGAACGACTACACCGAACTGAGTACCTACACGGGTGAGCTATG  
 AGAAGCGCCACGTTCCCGAAGSGAGAAAGCGGCACAGGTATCCGGTAAGCGCGAGGTTCGGAACAGGAGAGCGCAGGAGGAGCTTCCAGGGGGAACCGCTGGTATCTTTTATAGTCTCTGTGCG  
 GGTTTCGCAACCTCTGACTTGAAGCTCGAATTTTGTATGCTCTAGGGGGCGGAGCCTATGGAANAACCGCAACCGCGGCCCTTTACGGTTCCTGGCCCTTTTGTGGCCCTTTTGTGCTTGTGCTAC  
 ATGTTCTTCTCGGTTATCCCTGTATCTGTGATACCCGTTATTAACGCCTTTGAATGAGCTGATACCTGCTCGCCGACGCCCAACGACCGACCGGAGTCACTGAGCGGAGGAAGCGGAAG  
 CCGGCCAATATGCAAAACCGCTCTCCCGCGCGCTTGGCGTTTCAATTAATGAGCTGCGCAGCACTTTCCGACTTGGAAAGCGGGCAGTGA

**Fig. 9B**



## Replacement Sheet

Engineered gene III sequence in CM phage -- Nucleotide Sequence: SEQ ID. NO. 8;  
Amino Acid Sequence: SEQ ID. NOS. 9 and 25

SEQ ID. NO. 8  
KpnI Gene III leader Amber stop NotI Myc-tag BglII  
---TTAGTGGTACCTTTCTATTCTCACTCCGCT TAGGCTTGCGGTGGTGGCGCCGAGAACAAAACTCATCTCAGAAGAGGATCTGAGATCT AGATCTGGA

SEQ ID. NO. 9  
- L V V P F Y S H S A \* A C G G A A A E Q K L I S E E D L R S R S G

Gene III  
GGCGGT ACTGTTGAAAGTTGTTAGCAAAACCTCATACAGAAAATTTCATTACTAAGTCTGGAAAGACGACAAAACTTTAGATCGTTACGCT-----  
G G T V E S C L A K P H T E N S F T N V W K D D K T L D R Y A - -

Fig. 13B



SEQ ID NO. 10

[illegible]

**Fig. 15B**



# Replacement Sheet

## Engineered gene III Sequence in GMCT phage genome

SEQ ID. NO. 11

KpnI Gene III Leader

GR2 domain

--TTAGTGGTACCTTTCTATCTCACTCCGCT ACATCCCGCTGGAGGCGCTACAGTCAGAAACCATCGCCTGCGAATGAAGATCACAGAGCTGGATAAA

SEQ ID. NO. 12

-L V V P F Y S H S A T S R L E G L Q S E N H R L R M K I T E L D K

Myc-tag

GACTTGAAGAGGTCACCATGCAGCTGCAGGACGTCGGAGGTTGC GCGGCCGAGAACAAAACTGATCTCAGAAGAGGATCTGACGCGTGCT GGCGGC  
D L E E V T M Q L Q D V G G C A A E Q K L I S E E D L T R A G G

CT domain of Gene III

GGCTCTGGTGGTCTGGTGGCGGCTCTGAGGGTGGCGGCTCTGAGGGTGGCGGCTCTGAGGGTGGCGGTTCCGGTGGCGGCTCC  
G S G G S G G S E G G S E G G S E G G S E G G S E G G S E G G S  
GGTCCGGTGATTTGATGAAAAAATGGCAACGCTAATAAGGGGCTATGACCGAAATGCCGATGAAAACGCGCTACAGTCTGACGCTAAAGGCCAAA  
G S G D F D Y E K M A N A N K G A M T E N A D E N A L Q S D A K G K  
CTTGATTCTGCGCTACTGATTACGGTGTGCTATCGATGGTTTCATGGTGACGTTCCGGCCTTGCTAATGGTAATGGTGCTACTGGTGATTTGCTGGC  
L D S V A T D Y G A A I D G F I G D V S G L A N G N G A T G D F A G  
TCTAATCCCAATGGCTCAAGTCGGTGACGGTGATAATTCACCTTTAATGAATAATTCGGTCAATATTACCTTCCCTCAATCGGTTGAATGTCGC  
S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S L P Q S V E C R  
CCTTTTGTCTTTGGCGCTGGTAAACCATATGAATTTCTATTGATTGTGACAAAATAAACTTATCCGTTGGTGCTTTTGGCTTTTATATGTTGCCACC  
P F V F G A G K P Y E F S I D C D K I N L F R G V F A F L L Y V A T

Ascl S/D

TTTATGTATGATTTTCTACGTTTGCTAACATACTGCGTAATAAGGAGTCTTAATAA GCGCGCCCAACAATTCACAGTAAGGAGGTTTAATAA ATGAAA  
F M Y V F S T F A N I L R N K E S \* M K

OmpA leader

Gene III

AAGACAGCTATTGCGATTGCGAGTGGCACTGGCTGGTTTCGCTACCGTAGCGCAGGCT AGATCTGGAGGCGGT ACTGTTGAAAAGTTGTTAGCAAAA---  
K T A I A I A V A L A G F A T V A Q A R S G G G T V E S C L A K -

Fig. 19B



## Replacement Sheet

PABMD1 vector: sequence from AgeI to Sall - Nucleotide Sequence: SEQ ID. NO. 13  
Amino Acid Sequence: SEQ ID. NOS. 14 and 26

SEQ ID. NO. 13

lac promoter/lac O1      AgeI      EP      S/D  
AATTGTGACGGGATAACAATT ACCGGT TCTT TTAACCTTAG TAAGGAGG AATTAAAAA  
P8 Leader      HindIII      XbaI  
ATGAAAAAGTCTTTAGTCCTCAAGCCTCCGTAGCCGTGCTACCCCTCGTCCGATGCTAAGCTTCGCT TCTAGA

SEQ ID. NO. 14

M K K S L V L K A S V A V A T L V P M L S F A S R      SEQ ID. NO. 26

NotI      HA-tag

CGGGCCCGCT TATCCATACGACGTACCGACTACGCA GGAGGT CATCACCATCATCACCAT TAG AGATCT  
A A A Y P Y D V P D Y A G G H H H H H \*      R S  
His-tag      Amber stop      BglII

Gene 3

Sall

GGAGGCGGT ACTGTTGAAAGTTGTTTAGCAAAA ----- GCTAACATACTGCGTAATAAGGAGTCTTAA GTCGAC  
G G G T V E S C L A K ----- A N I L R N K E S \*

PABMD2 vector: sequence from AgeI to Sall

lac promoter/lac O1      AgeI      EP      S/D  
AATTGTGACGGGATAACAATT ACCGGT TCTT TTAACCTTAG TAAGGAGG AATTAAAAA  
pelB Leader      Nco I      PstI      XbaI

ATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGGGCCAGCCGCCCATGGCGCCCTGCAGGCCCTCTAGA  
M K Y L L P T A A A G L L L L A A Q P A M A A L Q A S R

SEQ ID. NO. 26

NotI

HA-tag

CGGGCCCGCT TATCCATACGACGTACCGACTACGCA GGAGGT CATCACCATCATCACCAT TAG AGATCT  
A A A Y P Y D V P D Y A G G H H H H H \*      R S  
His-tag      Amber stop      BglII

Gene 3

Sall

GGAGGCGGT ACTGTTGAAAGTTGTTTAGCAAAA ----- GCTAACATACTGCGTAATAAGGAGTCTTAA GTCGAC  
G G G T V E S C L A K ----- A N I L R N K E S \*

Fig. 22B





## Replacement Sheet

GR1 Sequence Range: 1 to 146

XbaI 10 20 30 40 50  
SEQ ID. NO. 15  
TCTAGAGGTGGAGGAGGTGAGGAGAAAGTCCCGGCTGTTGGAGAAGGAGAA  
SEQ ID. NO. 16  
S R G G G G E E K S R L L E K E N  
60 70 80 90 100  
CCGTGAAC TGGAAAAGATCATTTGCTGAGAAAGAGGAGCGGTGCTCTGAAC  
R E L E K I I A E K E R V S E  
110 120 130 140 AscI  
TGGGCCATCAACTCCAGTCTGTAGGAGGTTGTTAATAGGCGCGGCC  
L R H Q L Q S V G G C \* \*

GR2 Sequence Range: 1 to 140

XhoI 10 20 30 40 50  
SEQ ID. NO. 17  
TCTCGAGGAGGTGGTGGAAACATCCCGCCTGGAGGGCCTACAGTCAGAAAA  
SEQ ID. NO. 18  
S R G G G G T S R L E G L Q S E N  
60 70 80 90 100  
CCATCGCCTGCGAATGAAGATCACAGAGCTGGATAAAGACTTGAAGAGG  
H R L R M K I T E L D K D L E E  
110 120 130 NotI 140  
TCACCATGCAGCTGCAGGACGTCGGAGGTTGCGCGGCCGC  
V T M Q L Q D V G G C A A

Fig. 23



## Complete vector sequence of pABMX22

SEQ ID NO. 23

[illegible]

**Fig. 25B**

OIPE  
 FEB 17 2005  
 JIC99  
 TRADE MARK OFFICE

SEQ ID NO. 24

Fig. 26B